SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Fischhoff, David A
            Fuchs, Roy L
            Perlak, Frederick J

    (ii) TITLE OF INVENTION: Insect Resistant Plants

   (iii) NUMBER OF SEQUENCES: 54

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    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 09/027,998
        (B) FILING DATE: 23-FEB-1998
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Patterson, Melinda L
        (B) REGISTRATION NUMBER: 33,062
        (C) REFERENCE/DOCKET NUMBER: MOBT:195

    (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2615 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAGCGACTAT TATAATCATA CATATTTTCT ATTGGAATGA TTAAGATTCC AATAGAATAG        60

TGTATAAATT ATTTATCTTG AAAGGAGGGA TGCCTAAAAA CGAAGAACAT TAAAAACATA       120

TATTTGCACC GTCTAATGGA TTTATGAAAA ATCATTTAT CAGTTTGAAA ATTATGTATT        180

ATGATAAGAA AGGGAGGAAG AAAAATGAAT CCGAACAATC GAAGTGAACA TGATACAATA       240

AAAACTACTG AAAATAATGA GGTGCCAACT AACCATGTTC AATATCCTTT AGCGGAAACT       300

CCAAATCCAA CACTAGAAGA TTTAAATTAT AAAGAGTTTT TAAGAATGAC TGCAGATAAT       360

AATACGGAAG CACTAGATAG CTCTACAACA AAAGATGTCA TTCAAAAAGG CATTTCCGTA       420

GTAGGTGATC TCCTAGGCGT AGTAGGTTTC CCGTTTGGTG GAGCGCTTGT TTCGTTTTAT       480

ACAAACTTTT TAAATACTAT TTGGCCAAGT GAAGACCCGT GGAAGGCTTT TATGGAACAA       540

GTAGAAGCAT TGATGGATCA GAAAATAGCT GATTATGCAA AAAATAAAGC TCTTGCAGAG       600

TTACAGGGCC TTCAAAATAA TGTCGAAGAT TATGTGAGTG CATTGAGTTC ATGGCAAAAA       660

AATCCTGTGA GTTCACGAAA TCCACATAGC CAGGGGCGGA TAAGAGAGCT GTTTTCTCAA       720

GCAGAAAGTC ATTTTCGTAA TTCAATGCCT TCGTTTGCAA TTTCTGGATA CGAGGTTCTA       780

TTTCTAACAA CATATGCACA AGCTGCCAAC ACACATTTAT TTTTACTAAA AGACGCTCAA       840

ATTTATGGAG AAGAATGGGG ATACGAAAAA GAAGATATTG CTGAATTTTA TAAAAGACAA       900

CTAAAACTTA CGCAAGAATA TACTGACCAT TGTGTCAAAT GGTATAATGT TGGATTAGAT       960

AAATTAAGAG GTTCATCTTA TGAATCTTGG GTAAACTTTA ACCGTTATCG CAGAGAGATG      1020

ACATTAACAG TATTAGATTT AATTGCACTA TTTCCATTGT ATGATGTTCG GCTATACCCA      1080

AAAGAAGTTA AAACCGAATT AACAAGAGAC GTTTTAACAG ATCCAATTGT CGGAGTCAAC      1140

AACCTTAGGG GCTATGGAAC AACCTTCTCT AATATAGAAA ATTATATTCG AAAACCACAT      1200

CTATTTGACT ATCTGCATAG AATTCAATTT CACACGCGGT TCCAACCAGG ATATTATGGA      1260

AATGACTCTT TCAATTATTG GTCCGGTAAT TATGTTTCAA CTAGACCAAG CATAGGATCA      1320

AATGATATAA TCACATCTCC ATTCTATGGA AATAAATCCA GTGAACCTGT ACAAAATTTA      1380

GAATTTAATG GAGAAAAAGT CTATAGAGCC GTAGCAAATA CAAATCTTGC GGTCTGGCCG      1440

TCCGCTGTAT ATTCAGGTGT TACAAAAGTG GAATTTAGCC AATATAATGA TCAAACAGAT      1500

GAAGCAAGTA CACAAACGTA CGACTCAAAA AGAAATGTTG GCGCGGTCAG CTGGGATTCT      1560

ATCGATCAAT TGCCTCCAGA AACAACAGAT GAACCTCTAG AAAAGGGATA TAGCCATCAA      1620
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CTCAATTATG TAATGTGCTT TTTAATGCAG GGTAGTAGAG GAACAATCCC AGTGTTAACT      1680

TGGACACATA AAAGTGTAGA CTTTTTTAAC ATGATTGATT CGAAAAAAAT TACACAACTT      1740

CCGTTAGTAA AGGCATATAA GTTACAATCT GGTGCTTCCG TTGTCGCAGG TCCTAGGTTT      1800

ACAGGAGGAG ATATCATTCA ATGCACAGAA AATGGAAGTG CGGCAACTAT TTACGTTACA      1860

CCGGATGTGT CGTACTCTCA AAAATATCGA GCTAGAATTC ATTATGCTTC TACATCTCAG      1920

ATAACATTTA CACTCAGTTT AGACGGGGCA CCATTTAATC AATACTATTT CGATAAAACG      1980

ATAAATAAAG GAGACACATT AACGTATAAT TCATTTAATT TAGCAAGTTT CAGCACACCA      2040

TTCGAATTAT CAGGGAATAA CTTACAAATA GGCGTCACAG GATTAAGTGC TGGAGATAAA      2100

GTTTATATAG ACAAAATTGA ATTTATTCCA GTGAATTAAA TTAACTAGAA AGTAAAGAAG      2160

TAGTGACCAT CTATGATAGT AAGCAAAGGA TAAAAAAATG AGTTCATAAA ATGAATAACA      2220

TAGTGTTCTT CAACTTTCGC TTTTTGAAGG TAGATGAAGA ACACTATTTT TATTTTCAAA      2280

ATGAAGGAAG TTTTAAATAT GTAATCATTT AAAGGGAACA ATGAAAGTAG GAAATAAGTC      2340

ATTATCTATA ACAAAATAAC CATTTTTATA TAGCCAGAAA TGAATTATAA TATTAATCTT      2400

TTCTAAATTG ACGTTTTTCT AAACGTTCTA TAGCTTCAAG ACGCTTAGAA TCATCAATAT      2460

TTGTATACAG AGCTGTTGTT CCATCGAGT TATGTCCCAT TTGATTCGCT AATAGAACAA       2520

GATCTTTATT TTCGTTATAA TGATTGGTTG CATAAGTATG GCGTAATTTA TGAGGGCTTT      2580

TCTTTTCATC CAAAAGCCAA GTGTATTTCT CTGTA                                 2615
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 644 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr Glu
1               5                   10                  15

Asn Asn Glu Val Pro Thr Asn His Val Gln Tyr Pro Leu Ala Glu Thr
                20                  25                  30
```

Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35   40   45

Thr Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp
        50   55   60

Val Ile Gln Lys Gly Ile Ser Val Val Gly Asp Leu Leu Gly Val Val
65   70   75   80

Gly Phe Pro Phe Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Phe Leu
                85   90   95

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Glu Gln
                100   105   110

Val Glu Ala Leu Met Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asn Lys
        115   120   125

Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Val Glu Asp Tyr Val
        130   135   140

Ser Ala Leu Ser Ser Trp Gln Lys Asn Pro Val Ser Ser Arg Asn Pro
145   150   155   160

His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
                165   170   175

Phe Arg Asn Ser Met Pro Ser Phe Ala Ile Ser Gly Tyr Glu Val Leu
                180   185   190

Phe Leu Thr Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Phe Leu Leu
        195   200   205

Lys Asp Ala Gln Ile Tyr Gly Glu Glu Trp Gly Tyr Glu Lys Glu Asp
        210   215   220

Ile Ala Glu Phe Tyr Lys Arg Gln Leu Lys Leu Thr Gln Glu Tyr Thr
225   230   235   240

Asp His Cys Val Lys Trp Tyr Asn Val Gly Leu Asp Lys Leu Arg Gly
                245   250   255

Ser Ser Tyr Glu Ser Trp Val Asn Phe Asn Arg Tyr Arg Arg Glu Met
                260   265   270

Thr Leu Thr Val Leu Asp Leu Ile Ala Leu Phe Pro Leu Tyr Asp Val
        275   280   285

Arg Leu Tyr Pro Lys Glu Val Lys Thr Glu Leu Thr Arg Asp Val Leu
        290   295   300

Thr Asp Pro Ile Val Gly Val Asn Asn Leu Arg Gly Tyr Gly Thr Thr
305   310   315   320

Phe Ser Asn Ile Glu Asn Tyr Ile Arg Lys Pro His Leu Phe Asp Tyr
              325   330   335

Leu His Arg Ile Gln Phe His Thr Arg Phe Gln Pro Gly Tyr Tyr Gly
              340   345   350

Asn Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Ser Thr Arg Pro
              355   360   365

Ser Ile Gly Ser Asn Asp Ile Ile Thr Ser Pro Phe Tyr Gly Asn Lys
              370   375   380

Ser Ser Glu Pro Val Gln Asn Leu Glu Phe Asn Gly Glu Lys Val Tyr
385   390   395   400

Arg Ala Val Ala Asn Thr Asn Leu Ala Val Trp Pro Ser Ala Val Tyr
              405   410   415

Ser Gly Val Thr Lys Val Glu Phe Ser Gln Tyr Asn Asp Gln Thr Asp
              420   425   430

Glu Ala Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Val Gly Ala Val
              435   440   445

Ser Trp Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro
      450   455   460

Leu Glu Lys Gly Tyr Ser His Gln Leu Asn Tyr Val Met Cys Phe Leu
465   470   475   480

Met Gln Gly Ser Arg Gly Thr Ile Pro Val Leu Thr Trp Thr His Lys
              485   490   495

Ser Val Asp Phe Phe Asn Met Ile Asp Ser Lys Lys Ile Thr Gln Leu
              500   505   510

Pro Leu Val Lys Ala Tyr Lys Leu Gln Ser Gly Ala Ser Val Val Ala
              515   520   525

Gly Pro Arg Phe Thr Gly Gly Asp Ile Ile Gln Cys Thr Glu Asn Gly
      530   535   540

Ser Ala Ala Thr Ile Tyr Val Thr Pro Asp Val Ser Tyr Ser Gln Lys
545   550   555   560

Tyr Arg Ala Arg Ile His Tyr Ala Ser Thr Ser Gln Ile Thr Phe Thr
              565   570   575

Leu Ser Leu Asp Gly Ala Pro Phe Asn Gln Tyr Tyr Phe Asp Lys Thr
              580   585   590

Ile Asn Lys Gly Asp Thr Leu Thr Tyr Asn Ser Phe Asn Leu Ala Ser
              595   600   605

Phe Ser Thr Pro Phe Glu Leu Ser Gly Asn Asn Leu Gln Ile Gly Val
    610   615   620

Thr Gly Leu Ser Ala Gly Asp Lys Val Tyr Ile Asp Lys Ile Glu Phe
625   630   635   640

Ile Pro Val Asn

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

    Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr
    1   5   10   15

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAATCCNA ATAATCGNTC NGAACATGAT ACNATTAAAA CNACN   45

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGAACCCNA ACAACAGAAG TGAGCACGAC ACNATCAAGA CNACN   45

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 45 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAATCCNA ATAATCGGTC CGAACATGAT ACNATAAAAA CNACN   45

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 17 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAYCCNA AYAAYCG   17

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 17 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GARCAYGAYA CRATHAA   17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 45 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAACAATCC CAGTGTTTAG TAGGTAGCTA GCCAGATCTT TATTT   45

(2) INFORMATION FOR SEQ ID NO:10:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 45 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAATAAAGAT CTGGCTAGCT ACCTACTAAA CACTGGGATT GTTCC   45

(2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: not relevant
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

        Gly Thr Ile Pro Val Phe Ser Arg Leu Ala Arg Ser Leu Phe
        1   5   10

(2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 44 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTACAGGCGG AGATTAGTAG GTAGCTAGCC AGATCTTTAT TTTC   44

(2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 44 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAAATAAAG ATCTGGCTAG CTACCTACTA ATCTCCGCCT GTAA   44

(2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: not relevant
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

    Thr Gly Gly Asp Val Ala Ser Gln Ile Phe Ile Phe
    1   5   10

(2) INFORMATION FOR SEQ ID NO:15:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 45 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCAGTTTAG ACGGGGCTAG TAGGTAGCTA GCCAGATCTT TATTT   45

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 45 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATAAAGAT CTGGCTAGCT ACCTACTAGC CCCGTCTAAA CTGAG   45

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

    Leu Ser Leu Asp Gly Ala Ser Arg Leu Ala Arg Ser Leu Phe
    1   5   10

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTTATATAG ACAAAATTGA ATTTAGTAGG TAGCTAGCCA GATCTTTATT TT   52

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAAATAAAGA TCTGGCTAGC TACCTACTAA ATTCAATTTT GTCTATATAA AC   52

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Val Tyr Ile Asp Lys Ile Glu Phe Ser Arg Leu Ala Arg Ser Leu Phe
1   5   10   15

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TATAAAGAGT TTTTAAGAAT AACTGCAGAT AATAATA   37

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TATTATTATC TGCAGTTATT CTTAAAAACT CTTTATA   37

(2) INFORMATION FOR SEQ ID NO:23:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: not relevant
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

    Tyr Lys Glu Phe Leu Arg Ile Thr Ala Asp Asn Asn Thr
    1   5   10

(2) INFORMATION FOR SEQ ID NO:24:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 41 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATGGATGC AGATAATAAT ACGGAAGCAC TAGATAGCTC T   41

(2) INFORMATION FOR SEQ ID NO:25:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 41 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGAGCTATCT AGTGCTTCCG TATTATTATC TGCATCCATG G   41

(2) INFORMATION FOR SEQ ID NO:26:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: not relevant
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

        Met Asp Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser
        1   5   10

(2) INFORMATION FOR SEQ ID NO:27:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 41 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCATGCTAGG AGTAGTAGGT TTCCCGTTTG TGGAGCGCTT G   41

(2) INFORMATION FOR SEQ ID NO:28:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 41 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAGCGCTCC ACAAACGGGA AACCTACTAC TCCTAGCATG G

(2) INFORMATION FOR SEQ ID NO:29:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 13 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: not relevant
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

        Met Leu Gly Val Val Gly Phe Pro Phe Val Glu Arg Leu
        1   5   10

(2) INFORMATION FOR SEQ ID NO:30:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCATGGCAAT TTGGCCAAGT GAAGAC   26

(2) INFORMATION FOR SEQ ID NO:31:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 26 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCTTCACTT GGCCAAATTG CCATGG   26

(2) INFORMATION FOR SEQ ID NO:32:

        (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

    Met Ala Ile Trp Pro Ser Glu Asp
    1   5

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 661 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAGCTTGCAT GCCTGCAGGT CCGATGTGAG ACTTTTCAAC AAAGGGTAAT ATCCGGAAAC   60

CTCCTCGGAT TCCATTGCCC AGCTATCTGT CACTTTATTG TGAAGATAGT GGAAAAGGAA   120

GGTGGCTCCT ACAAATGCCA TCATTGCGAT AAAGGAAAGG CCATCGTTGA AGATGCCTCT   180

GCCGACAGTG GTCCCAAAGA TGGACCCCCA CCCACGAGGA GCATCGTGGA AAAAGAAGAC   240

GTTCCAACCA CGTCTTCAAA GCAAGTGGAT TGATGTGATG GTCCGATGTG AGACTTTTCA   300

ACAAAGGGTA ATATCCGGAA ACCTCCTCGG ATTCCATTGC CCAGCTATCT GTCACTTTAT   360

TGTGAAGATA GTGGAAAAGG AAGGTGGCTC CTACAAATGC CATCATTGCG ATAAAGGAAA   420

GGCCATCGTT GAAGATGCCT CTGCCGACAG TGGTCCCAAA GATGGACCCC CACCCACGAG   480

GAGCATCGTG GAAAAGAAG ACGTTCCAAC CACGTCTTCA AAGCAAGTGG ATTGATGTGA   540

TATCTCCACT GACGTAAGGG ATGACGCACA ATCCCACTAT CCTTCGCAAG ACCCTTCCTC   600

TATATAAGGA AGTTCATTTC ATTTGGAGAG GACACGCTGA CAAGCTGACT CTAGCAGATC   660

T   661

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: not relevant
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

    Met Xaa Pro Xaa Thr Arg Ala Leu Asp Asp Thr Ile Lys Lys Asp Val
    1   5   10   15

    Ile Gln Lys

(2) INFORMATION FOR SEQ ID NO:35:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGAACATGGT TAGTTGG   17

(2) INFORMATION FOR SEQ ID NO:36:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGGTGATCT CTAGGCG   17

(2) INFORMATION FOR SEQ ID NO:37:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGAACAACCT TCTCTAATAT   20

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGAAYCCNA AYAAYCG   17

(2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GARCAYGAYA CYATHAA   17

(2) INFORMATION FOR SEQ ID NO:40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GATTGTTCGG ATCCATGGTT CTTCCTCCCT   30

(2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAGTAGGTAG CTAGCCA   17

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCTGGCTA GCTACCTACT A   21

(2) INFORMATION FOR SEQ ID NO:43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGTATTATTA TCTGCATCCA TGGTTCTTCC TCCCT   35

(2) INFORMATION FOR SEQ ID NO:44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATTATTATCT GCAGTTATTC TTAAAAACTC TTTAT   35

(2) INFORMATION FOR SEQ ID NO:45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACTTGGCC AAATTGCCAT GGTATTTAAA AAGTTTGT   38

(2) INFORMATION FOR SEQ ID NO:46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGATAAGAA AGGGAGGAAG AAAAATGAAT CCGAACAATC GAAGTGAACA TGATACAATA   60

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid

(C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

    Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile
    1   5   10

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGGATTCATT TTAGATCTTC CTCCCTT   27

(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTTATATAG ACAAAATTGA ATTTATTCCA GTGAATTAAA TTAACTAGAA AGTAAAGAAG   60

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn
1   5   10

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTTCTAGTT AAAGATCTTT AATTCACTG   29

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCAAATCCAA CACTAGAAGA TTTAAATTAT AAAGAGTTTT TAAGAATGAC TGCAGATAAT   60

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
1               5                   10                  15

Thr Ala Asp Asn
            20
```

(2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCTGCAGTC ATTGTAGATC TCTCTTTATA ATTT   34